

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 07:24:35 ; Search time 50 Seconds
(without alignments)
365.311 Million cell updates/sec

Title: US-09-895-298A-83

Perfect score: 190
Sequence: 1 MMNFQPPSKAMRASQWTF.....HDGSLDLRSRRSYQEGNPRA 190

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 4

Total number of hits satisfying chosen parameters: 121138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	4.2	335	2 H75029	hypothetical prote
2	8	4.2	351	2 T22861	hypothetical prote
3	8	4.2	752	2 E97011	ATPase with chap
4	7	3.7	115	2 I51064	somatosatin II pr
5	7	3.7	136	2 T38482	hypothetical prote
6	7	3.7	151	2 JN0569	single-stranded mi
7	7	3.7	170	2 T31967	hypothetical prote
8	7	3.7	180	2 D90569	hypothetical prote
9	7	3.7	202	2 AB1527	hypothetical prote
10	7	3.7	202	2 AH1169	hypothetical prote
11	7	3.7	214	2 S49599	probable permease
12	7	3.7	215	2 B64305	hypothetical prote
13	7	3.7	241	2 D64498	hypothetical prote
14	7	3.7	244	2 A55541	heterocyst maturat
15	7	3.7	244	2 A12269	heterocyst specifi
16	7	3.7	245	2 A90527	hypothetical prote
17	7	3.7	259	2 S36410	translation initia
18	7	3.7	324	2 F69287	UDP-glucose dehydr
19	7	3.7	327	2 T27484	hypothetical prote
20	7	3.7	330	1 B70177	conserved hypotet
21	7	3.7	338	2 S56333	carbon-phosphorus
22	7	3.7	338	2 G91264	hypothetical prote
23	7	3.7	338	2 D86105	hypothetical prote
24	7	3.7	340	2 T03220	probable pteridine
25	7	3.7	355	2 T12104	NADH2 dehydrogenas
26	7	3.7	355	2 T12032	NADH2 dehydrogenas
27	7	3.7	355	2 T13830	NADH2 dehydrogenas
28	7	3.7	355	2 T13831	NADH2 dehydrogenas
29	7	3.7	355	2 T11601	NADH2 dehydrogenas

30	7	3.7	355	2 T13833	NADH2 dehydrogenas
31	7	3.7	355	2 T13861	NADH2 dehydrogenas
32	7	3.7	355	2 T13862	NADH2 dehydrogenas
33	7	3.7	355	2 T12029	NADH2 dehydrogenas
34	7	3.7	355	2 T12031	NADH2 dehydrogenas
35	7	3.7	355	2 T12028	NADH2 dehydrogenas
36	7	3.7	355	2 T12023	NADH2 dehydrogenas
37	7	3.7	355	2 T12034	NADH2 dehydrogenas
38	7	3.7	355	2 T12114	NADH2 dehydrogenas
39	7	3.7	355	2 T12111	NADH2 dehydrogenas
40	7	3.7	355	2 T12033	NADH2 dehydrogenas
41	7	3.7	355	2 T12118	NADH2 dehydrogenas
42	7	3.7	355	2 T12119	NADH2 dehydrogenas
43	7	3.7	355	2 T12112	NADH2 dehydrogenas
44	7	3.7	355	2 T12026	NADH2 dehydrogenas
45	7	3.7	355	2 T12154	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1
H75029
hypothetical protein PAB1174 - Pyrococcus abyssi (strain Orsay)
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C/Accession: H75029
R/anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A/Reference number: A75001
A/Accession: H75029
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-335 <KAW>
A/Cross-references: GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50678.1; PID:g545
A/Experimental source: strain Orsay
C/Genetics:
A/Gene: PAB1174
C/Superfamily: conserved hypothetical protein MTH887

Query Match 4.2%; Score 8; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 ILTLIVLI 101
Db 158 ILTLIVLI 165

RESULT 2
T22861
hypothetical protein F57G4.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T22861
R/Ainscough, R.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19629
A/Accession: T22861
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-351 <WIL>
A/Cross-references: EMBL:Z81554; PIDN:CAB04503.1; GSPDB:GN00023; CESP:F57G4.4
A/Experimental source: clone F57G4
C/Genetics:
A/Gene: CESP:F57G4.4
A/Map position: 5
A/Introns: 65/2; 93/2; 149/2; 288/3

Query Match 4.2%; Score 8; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 DGSILRS 179
| | | | |
Db 55 DGSILRS 62

RESULT 3

E97011
ATPase with chaperon activity, two ATP-binding domains, ClpC orthologs CAC0904 [Imported
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: E97011
R: Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clp
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97011
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-752 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK78880.1; PID:915023802; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0904
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 4.2%; Score 8; DB 2; Length 752;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 124 INEGDK 131
| | | | |
Db 678 INEGDK 685

102-b

RESULT 4

IS1064
somatostatin II precursor - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: IS1064
R: Moore, C.A.; Kittilson, J.D.; Dahl, S.K.; Sheridan, M.A.
Gen. Comp. Endocrinol. 98, 253-261, 1995
A:Title: Isolation and characterization of a cDNA encoding for preprosomatostatin containi
A:Reference number: IS1064; MUID:95354921; PMID:7628684
A:Accession: IS1064
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-115 <MOO>
A:Cross-references: EMBL:U32471; NID:9975344; PIDN:AAC59695.1; PID:9975345
C:Superfamily: somatostatin

Query Match 3.7%; Score 7; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 LDLSRR 181
| | | | |
Db 30 LDLSRR 36

RESULT 5

T38482
hypothetical protein SPAC29A4.07 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38482
R: Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z21796
A:Accession: T38482
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-136 <BRO>
A:Cross-references: EMBL:Z97210; PIDN:CAB10134.1; GSPDB:GN00066; SPDB:SPAC29A4.07
A:Experimental source: strain 972h-; cosmid c29A4
C:Genetics:
A:Gene: SPDB:SPAC29A4.07
A:Map position: 1

Query Match 3.7%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 125 INEGDK 131
| | | | |
Db 40 INEGDK 46

RESULT 6

JN0569
single-stranded mitochondrial DNA-binding protein precursor - rat
N:Alternate names: DNA-binding protein p16; helix-stabilizing protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
C:Accession: JN0569; S13264
R: Tiranti, V.; Rocchi, M.; Didonato, S.; Zeviani, M.
Gene 126, 219-225, 1993
A:Title: Cloning of human and rat cDNAs encoding the mitochondrial single-stranded DN
A:Reference number: JN0568; MUID:93246247; PMID:8482537
A:Accession: JN0569
A:Molecule type: mRNA
A:Residues: 1-151 <TIR>
A:Cross-references: GB:M94557; NID:g205543; PIDN:AA67315.1; PID:g205544
A:Note: the authors translated the codon AAT for residue 70 as Ser, GAA for residue 7
s Met

R:Hoek, G.D.; Payco, P.A.; Ledwith, B.J.; van Tuyle, G.C.

Arch. Biochem. Biophys. 282, 116-124, 1990

A:Title: Structural and functional studies of the rat mitochondrial single strand DNA
A:Reference number: S13264; MUID:91024186; PMID:2221914
A:Accession: S13264

A:Molecule type: protein
A:Residues: 17-46 <HOK>

C:Comment: This protein is used to stabilize the displaced single strand of of DNA du
C:Superfamily: single-stranded DNA-binding protein; single-stranded DNA-binding prote
C:Keywords: DNA binding; DNA replication; mitochondrion
F:1-16/Domain: transit peptide (mitochondrion) #status predicted <SIG>
F:17-148/Product: single-stranded mitochondrial DNA-binding protein #status predicted
F:46-130/Domain: single-stranded DNA-binding protein homology <SSD>

Query Match 3.7%; Score 7; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 151 SSVLVR 157
| | | | |
Db 22 SSVLVR 28

RESULT 7

T31967
hypothetical protein C33C12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31967
R: Gatung, S.; Scheet, P.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid C33C12.
A:Reference number: Z21105
A:Accession: T31967
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-170 <GAT>
A:Cross-references: EMBL:AF016662; PIDN:AAB66062.1; GSPDB:GN00020; CESP:C33C12.2
A:Experimental source: strain Bristol N2; clone C33C12

C:Genetics:
A:Gene: CESP:C33C12.2
A:Map position: 2
A:Introns: 69/3; 113/2

Query Match 3.7%; Score 7; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 133 FLIEKLI 139
|||||||
DB 56 FLIEKLI 62

RESULT 8
D90569
hypothetical protein MYPV_4600 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: D90569
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2143-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: D90569
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-180 <KUR>
A:Cross-references: GB:AL445566; PID:g14089874; PIDN:CAC13633.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV_4600
A:Genetic code: SGC3

Query Match 3.7%; Score 7; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 135 IEKLIK 141
|||||||
DB 142 IEKLIK 148

RESULT 9
AB1527
hypothetical protein lin0754 [Imported] - Listeria innocua (strain C11p11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB1527
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AB1527
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <GIA>
A:Cross-references: GB:AL592022; PIDN:CAC95986.1; PID:g16413205; GSPDB:GN00178
A:Experimental source: strain C11p11262
C:Genetics:
A:Gene: lin0754

Query Match 3.7%; Score 7; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 171 HDGSIDL 177
|||||||
DB 62 HDGSIDL 68

RESULT 10
AH1169
hypothetical protein lmo0760 [Imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AH1169
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maltournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <GIA>
A:Cross-references: GB:NC_003210; PIDN:CAC98838.1; PID:g16410149; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0760

Query Match 3.7%; Score 7; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 171 HDGSIDL 177
|||||||
DB 62 HDGSIDL 68

RESULT 11
S49599
probable permease nisc - Lactococcus lactis
C:Species: Lactococcus lactis
C:Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 15-Oct-1999
C:Accession: S49599
R:Immonen, T.; Paulin, L.; Saris, P.
submitted to the EMBL Data Library, January 1994
A:Description: The gntxyz region in the conjugative nisin-sucrose transposon of Lacto
n.
A:Reference number: S49597
A:Accession: S49599
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-214 <IMM>
A:Cross-references: EMBL:Z29363; NID:g575300; PIDN:CA82549.1; PID:g575303
C:Superfamily: Lactococcus lactis probable permease nisc

Query Match 3.7%; Score 7; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 FLFFPS 28
|||||||
DB 96 FLFFPS 102

RESULT 12
B64305
hypothetical protein MJ0042 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C:Accession: B64305
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc

A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64305
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <BUL>
A;Cross-references: GB:067462; GB:L77117; NID:g1590835; PIDN:AAB98028.1; PID:g1498802; T
C;Genetics:
A;Map position: REV42527-41880

Query Match 3.7%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LIEKLIK 140
|||||
DB 198 LIEKLIK 204

RESULT 13
D64498
hypothetical protein MJ1589 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: D64498
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64498
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-241 <BUL>
A;Cross-references: GB:067599; GB:L77117; NID:g2826435; PIDN:AAB99617.1; PID:g1500485; T
C;Genetics:
A;Map position: FOR1561658-1562383

Query Match 3.7%; Score 7; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 99 VLITTYL 105
|||||
DB 168 VLITTYL 174

RESULT 14
A55541
heterocyst maturation protein devA - Anabaena sp. (strain PCC 7120)
C;Species: Anabaena sp.
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Feb-2001
C;Accession: A55541; S38423
R;Maidener, I.; Fiedler, G.; Ernst, A.; Fernandez-Pinas, F.; Wolk, C.P.
J. Bacteriol. 176, 7543-7549, 1994
A;Title: Characterization of devA, a gene required for the maturation of proheterocysts
A;Reference number: A55541; MUID:95095923; PMID:8002578
A;Accession: A55541
A;Molecule type: DNA
A;Residues: 1-244 <MAL>
A;Cross-references: EMBL:X75422; NID:g407772; PIDN:CA53174.1; PID:g407773
C;Genetics:
A;Gene: devA
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;26-222/Domain: ATP-binding cassette homology <ABC>
F;43-50/Region: nucleotide-binding motif A (P-loop)

Query Match 3.7%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 RSVQEGN 187
|||||
DB 60 RSVQEGN 66

RESULT 15
AI2269
heterocyst specific ABC-transporter, ATP-binding chain devA [imported] - Nostoc sp. (AI2269)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AI2269
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2269
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-244 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA875411.1; PID:g17132846; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: devA
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homolo

Query Match 3.7%; Score 7; DB 2; Length 244;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 RSVQEGN 187
|||||
DB 60 RSVQEGN 66

RESULT 16
A90527
hypothetical protein MYPV_1210 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: A90527
R;Chamblaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallison, F.; Moszer,
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p
A;Reference number: A9512; MUID:21267165; PMID:11353084
A;Accession: A90527
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-245 <KUR>
A;Cross-references: GB:AL445566; PID:g14089534; PIDN:CAC13294.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPV_1210
A;Genetic code: SGC3

Query Match 3.7%; Score 7; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 TLIVLIT 102
|||||
DB 223 TLIVLIT 229

RESULT 17
S36410
translation initiation factor IF-2, chloroplast - red alga (Cyanidium caldarium) chlo
C;Species: chloroplast Cyanidium caldarium
C;Date: 06-Jan-1995 #sequence_revision 24-Oct-1997 #text_change 02-Feb-2001
C;Accession: S36410; S70822
R;Kosirzawa, M.; Zetsche, K.
submitted to the EMBL Data Library, June 1992

A:Reference number: S36410
A:Accession: S36410
A:Molecule type: DNA
A:Residues: 1-259 <KOS>
A:Cross-references: EMBL:X66698; NID:g396522; PID:g396523
A:Experimental source: strain 14-1-1
R:Kostrzewa, M.; Zetsche, K.
Plant Mol. Biol. 23, 67-76, 1993
A:Title: Organization of plastid-encoded ATPase genes and flanking regions including hom
A:Reference number: S39512; MUID:94033298; PMID:8219057
A:Accession: S70822
A:Molecule type: DNA
A:Residues: 88-259 <KOF>
A:Cross-references: EMBL:X66698
A:Experimental source: strain 14-1-1
A:Note: the source is designated as *Galdieria sulphuraria*
C:Genetics:
A:Gene: *infB*
A:genome: chloroplast
C:Superfamily: translation initiation factor IF-2; translation elongation factor Tu hom
C:Keywords: chloroplast; GTP binding; nucleotide binding; P-loop; protein biosynthesis
F:174-259/Domain: translation elongation factor Tu homology (fragment) <EFL>
F:180-187/Region: nucleotide-binding motif A (P-loop)

Query Match 3.7%; Score 7; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 LIEKLIK 140
|||||
DB 189 LIEKLIK 195

RESULT 18
F69287
UDP-glucose dehydrogenase (ugd-1) homolog - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C:Accession: F69287
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: F69287
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-324 <KLE>
A:Cross-references: GB:AE001084; GB:AE000782; NID:g2689407; PIDN:AAB90929.1; PID:g265033
C:Superfamily: GDPmannose dehydrogenase

Query Match 3.7%; Score 7; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 DGSIDL 178
|||||
DB 89 DGSIDL 95

RESULT 19
T27484
hypothetical protein Y94A7B.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T27484
R:Kershaw, J.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z20373
A:Accession: T27484

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-327 <WIL>
A:Cross-references: EMBL:AL023856; PIDN:CAA19567.1; GSPDB:GN00023; CESP:Y94A7B.5
A:Experimental source: clone Y94A7B
C:Genetics:
A:Gene: CESP:Y94A7B.5
A:Map position: 5
A:Introns: 104/1; 245/3
C:Superfamily: *Caenorhabditis* hypothetical protein C4967.2

Query Match 3.7%; Score 7; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 LTLIVL 101
|||||
DB 197 LTLIVL 203

RESULT 20
B70177
conserved hypothetical protein BB0619 - Lyme disease spirochete
C:Species: *Borrelia burgdorferi* (Lyme disease spirochete)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C:Accession: B70177
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70177
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-330 <KLE>
A:Cross-references: GB:AE001163; GB:AE000783; NID:g2688541; PIDN:AAC66977.1; PID:g268
A:Experimental source: strain B31
C:Superfamily: Mycoplasma conserved hypothetical protein MG190

Query Match 3.7%; Score 7; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 FLIEKLI 139
|||||
DB 139 FLIEKLI 145

RESULT 21
S56333
carbon-phosphorus lyase phnd - *Escherichia coli* (strain K-12)
C:Species: *Escherichia coli*
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002
C:Accession: S56333; H65219; E35718
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:95334362; PMID:7610040
A:Accession: S56333
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-338 <BUR>
A:Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97004.1; PID:g536949
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H65219
A:Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA
A;Residues: 1-338 <BLAT>
A;Cross-references: GB:AE000482; GB:U00096; NID:g2367349; PIDN:AAC77066.1; PID:g1790543;
A;Experimental source: strain K-12, substrain MG1655
R;Chen, C.M.; Ye, Q.Z.; Zhu, Z.; Wanner, B.L.; Walsh, C.T.
J. Biol. Chem. 265, 4461-4471, 1990
A;Title: Molecular biology of carbon-phosphorus bond cleavage. Cloning and sequencing of
A;Reference number: A35718; MUID:90170953; PMID:2155230
A;Accession: E35718
A;Molecule type: DNA
A;Residues: 1-311,'A',313-338 <CHE>
A;Cross-references: GB:J05260; NID:g147192; PIDN:AAA24340.1; PID:g147197
C;Genetics:
A;Gene: phnd

Query Match 3.7%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LQDMEKK 147
|||||
Db 54 LQDMEKK 60

RESULT 22
G91264
hypothetical protein ECS5087 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G91264
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-338 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA838510.1; PID:g13364564; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECS5087

Query Match 3.7%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LQDMEKK 147
|||||
Db 54 LQDMEKK 60

RESULT 23
D86105
hypothetical protein phnd [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D86105
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.T.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: AB5480; MUID:21074935; PMID:11206551
A;Accession: D86105
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-338 <STO>
A;Cross-references: GB:AE005174; NID:g12519072; PIDN:AAG59304.1; GSPDB:GN00145; UWGP:257
C;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: phnd

Query Match 3.7%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LQDMEKK 147
|||||
Db 54 LQDMEKK 60

RESULT 24
T03220
probable pteridine-dependent dioxygenase - Streptomyces hygroscopicus
C;Species: Streptomyces hygroscopicus
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 22-Oct-1999
C;Accession: T03220
R;Ruan, X.; Stassi, D.; Lax, S.; Katz, L.
Gene 203, 1-9, 1997
A;Title: A second type-I PKS gene cluster isolated from Streptomyces hygroscopicus AT
A;Reference number: Z14848; MUID:98085969; PMID:9426000
A;Accession: T03220
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-340 <RUA>
A;Cross-references: EMBL:AF007101; NID:g2624946; PIDN:AAC38060.1; PID:g2624947
A;Experimental source: ATCC 29253

Query Match 3.7%; Score 7; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 NPSSLVL 155
|||||
Db 2 NPSSLVL 8

RESULT 25
T12104
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 (isolate High Tatras Slovakia)
C;Species: mitochondrion Carabus 11mel
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C;Accession: T12104; T12106
R;Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A;Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A;Reference number: Z17381
A;Accession: T12104
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-355 <IMD>
A;Cross-references: EMBL:AB017472; PIDN:BAA33188.1
A;Experimental source: isolate High Tatras Slovakia; adult; thorax muscle
A;Accession: T12106
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-122,'L',124-355 <IM2>
A;Cross-references: EMBL:AB017473; PIDN:BAA33189.1
A;Experimental source: isolate Zilina Slovakia; adult; thorax muscle
C;Genetics:
A;Genome: mitochondrion
A;Note: ND5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||
Db 157 FIFLLFF 163

RESULT 26

T12032
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 (isolate Mt. Khumaratkhek Russia)
C:Species: mitochondrion Carabus cibratus
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12032
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
E:Yura 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endo
A:Reference number: 217381
A:Accession: T12032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017461; PIDN:BAA33177.1
A:Experimental source: isolate Mt. Khumaratkhek Russia; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 27
T13830
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Acoprolabrus gehinli mitochondri
C:Species: mitochondrion Acoprolabrus gehinli
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13830
R:Su, Z.H.; Tomihaga, O.; Okamoto, M.; Osawa, S.
Mol. Biol. Evol. 15, 1026-1039, 1998
A:Title: Origin and diversification of hindwingless Damaster ground beetles within the J
A:Reference number: Z17319; MUID:98384842; PMID:9718730
A:Accession: T13830
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <SUZ>
A:Cross-references: EMBL:D50339; NID:g1000905; PIDN:BAA08874.1; PID:g1438078
A:Experimental source: adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 28
T13831
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Acoprolabrus gehinli ssp. radiat
C:Species: mitochondrion Acoprolabrus gehinli ssp. radiatocostatus
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13831
R:Su, Z.H.; Tomihaga, O.; Okamoto, M.; Osawa, S.
Mol. Biol. Evol. 15, 1026-1039, 1998
A:Title: Origin and diversification of hindwingless Damaster ground beetles within the J
A:Reference number: Z17319; MUID:98384842; PMID:9718730
A:Accession: T13831
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-355 <SUZ>
A:Cross-references: EMBL:D50429; PIDN:BAA08925.1
A:Experimental source: adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 29
T11601
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Aristocarabus viridifossulatu
C:Species: mitochondrion Aristocarabus viridifossulatus
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T11601
R:Imura, Y.; Zhou, H.Z.; Okamoto, M.; Su, Z.H.; Osawa, S.
submitted to the EMBL Data Library, January 1998
A:Description: Phylogenetic relationships of some Chinese beetles belonging to the su
s.
A:Reference number: Z17298
A:Accession: T11601
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB010718; PIDN:BAA24681.1
A:Experimental source: adult; isolate Baoxing-Sichuan; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 30
T13833
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Asthenocarabus opaculus mitoc
C:Species: mitochondrion Asthenocarabus opaculus
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13833
R:Su, Z.H.; Ohama, T.; Okada, T.S.; Nakamura, K.; Ishikawa, R.; Osawa, S.
J. Mol. Evol. 42, 124-129, 1996
A:Title: Phylogenetic relationships and evolution of the Japanese Carabinae ground be
A:Reference number: Z17787; MUID:97077297; PMID:8919864
A:Accession: T13833
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <SUZ>
A:Cross-references: EMBL:D50340; NID:g1000901; PIDN:BAA08875.1; PID:g1438079
A:Experimental source: adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||||

Db 157 FIFLLFF 163

RESULT 31
T13861
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Campalita chinense mitochondrion
C:Species: mitochondrion Campalita chinense
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13861
R:Su, Z.H.; Ohama, T.; Okada, T.S.; Nakamura, K.; Ishikawa, R.; Osawa, S.
J. Mol. Evol. 42, 124-129, 1996
A:Title: Phylogenetic relationships and evolution of the Japanese Carabinae ground beetle
A:Reference number: Z17787; MUID:97077297; PMID:8919864
A:Accession: T13861
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <SUZ>
A:Cross-references: EMBL:D50343; NID:g1000915; PIDN:BAA08878.1; PID:g1438082
A:Experimental source: adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||||

Db 157 FIFLLFF 163

RESULT 32
T13862
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus conciliator mitochondrion
C:Species: mitochondrion Carabus conciliator
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
C:Accession: T13862
R:Su, Z.H.; Ohama, T.; Okada, T.S.; Nakamura, K.; Ishikawa, R.; Osawa, S.
J. Mol. Evol. 42, 124-129, 1996
A:Title: Phylogenetic relationships and evolution of the Japanese Carabinae ground beetle
A:Reference number: Z17787; MUID:97077297; PMID:8919864
A:Accession: T13862
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <SUZ>
A:Cross-references: EMBL:D50344; NID:g1000919; PIDN:BAA08879.1; PID:g1438083
A:Experimental source: adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||||

Db 157 FIFLLFF 163

RESULT 33
T12029
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus concolor mitochondrion
C:Species: mitochondrion Carabus concolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12029

R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A:Reference number: Z17381
A:Accession: T12029
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017458; PIDN:BAA33174.1
A:Experimental source: isolate Furka-Pass Swiss; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||||

Db 157 FIFLLFF 163

RESULT 34
T12031
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus cribratus mitochondrion
C:Species: mitochondrion Carabus cribratus
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12031
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A:Reference number: Z17381
A:Accession: T12031
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017460; PIDN:BAA33176.1
A:Experimental source: isolate Artvin Turkey; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 FIFLLFF 26
|||||||

Db 157 FIFLLFF 163

RESULT 35
T12028
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus falmalrei heteromorph
C:Species: mitochondrion Carabus falmalrei heteromorphus
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12028
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A:Reference number: Z17381
A:Accession: T12028
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017455; PIDN:BAA33171.1
A:Experimental source: isolate Champorcer Italy N01; adult; thorax muscle
C:Genetics:

A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
|||||
Db 157 FIFLFF 163

RESULT 36

T12023

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus fairmairei pelvicius mitc

C:Species: mitochondrion Carabus fairmairei pelvicius

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002

C:Accession: T12023; T12024

R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.

Elytra 26, 223-248, 1998

A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endc

A:Reference number: 217381

A:Accession: T12023

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <IMD>

A:Cross-references: EMBL:AB017449; PIDN:BAA33165.1

A:Experimental source: isolate Colle di Bellino Italy NO1; adult; thorax muscle

A:Accession: T12024

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-234, 'L', 236-355 <IM2>

A:Cross-references: EMBL:AB017450; PIDN:BAA33166.1

A:Experimental source: isolate Colle di Bellino Italy NO2; adult; thorax muscle

C:Genetics:

A:Genome: mitochondrion

A:Note: ND5

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
|||||
Db 157 FIFLFF 163

RESULT 37

T12034

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus hortensis mitochondrion

C:Species: mitochondrion Carabus hortensis

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002

C:Accession: T12034

R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.

Elytra 26, 223-248, 1998

A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endc

A:Reference number: 217381

A:Accession: T12034

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <IMD>

A:Cross-references: EMBL:AB017463; PIDN:BAA33179.1

A:Experimental source: isolate Innsbruck Austria; adult; thorax muscle

C:Genetics:

A:Genome: mitochondrion

A:Note: ND5

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
|||||
Db 157 FIFLFF 163

RESULT 38

T12114

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus latreilleanus mitoch

C:Species: mitochondrion Carabus latreilleanus

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002

C:Accession: T12114

R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.

Elytra 26, 223-248, 1998

A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e

A:Reference number: 217381

A:Accession: T12114

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <IMD>

A:Cross-references: EMBL:AB017478; PIDN:BAA33194.1

A:Experimental source: isolate Champorcer Italy; adult; thorax muscle

C:Genetics:

A:Genome: mitochondrion

A:Note: ND5

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
|||||
Db 157 FIFLFF 163

RESULT 39

T12111

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus latro minshanensis ml

C:Species: mitochondrion Carabus latro minshanensis

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002

C:Accession: T12111

R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.

Elytra 26, 223-248, 1998

A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e

A:Reference number: 217381

A:Accession: T12111

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <IMD>

A:Cross-references: EMBL:AB017476; PIDN:BAA33192.1

A:Experimental source: isolate Jiuhaigou Sichuan China; adult; thorax muscle

C:Genetics:

A:Genome: mitochondrion

A:Note: ND5

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio

Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 FIFLFF 26
|||||
Db 157 FIFLFF 163

RESULT 40

T12033

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus porrectangulus mitochondrion
C:Species: mitochondrion Carabus porrectangulus
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12033
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endo
A:Reference number: Z17381
A:Accession: T12033
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017462; PIDN:BA33178.1
A:Experimental source: Isolate Gumushane Turkey; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 41
T12118
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus porrecticollis mitochondrion
C:Species: mitochondrion Carabus porrecticollis
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T12118
R:Kim, C.G.; Tomioka, O.; Su, Z.H.; Osawa, S.
submitted to the EMBL Data Library, January 1999
A:Description: Origin and diversification of Euleptocarabus porrecticollis (Coleoptera,
A:Reference number: Z17425
A:Accession: T12118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <KIM>
A:Cross-references: EMBL:AB022555; PIDN:CAB19781.1
A:Experimental source: collection site: Kakunodate Akita Pref.; isolate 1; adult; thorax
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 42
T12119
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus porrecticollis mitochondrion
C:Species: mitochondrion Carabus porrecticollis kansalensis
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002
C:Accession: T12119
R:Kim, C.G.; Su, Z.H.; Osawa, S.
submitted to the EMBL Data Library, January 1999
A:Description: Origin and diversification of Euleptocarabus porrecticollis (Coleoptera,
A:Reference number: Z17426
A:Accession: T12119
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-355 <KIM>
A:Cross-references: EMBL:AB022571; PIDN:CAB1979.1
A:Experimental source: collection site: Kaga Ishikawa Pref.; isolate 18; adult; thorax
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 43
T12112
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus pusio mitochondrion
C:Species: mitochondrion Carabus pusio
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12112
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A:Reference number: Z17381
A:Accession: T12112
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017477; PIDN:BA33193.1
A:Experimental source: isolate Gonggaling Sichuan China; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 FIFLFF 26
Db 157 FIFLFF 163
RESULT 44
T12026
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus putzeysianus germanae
C:Species: mitochondrion Carabus putzeysianus germanae
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002
C:Accession: T12026
R:Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.
Elytra 26, 223-248, 1998
A:Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on e
A:Reference number: Z17381
A:Accession: T12026
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-355 <IMU>
A:Cross-references: EMBL:AB017453; PIDN:BA33169.1
A:Experimental source: isolate Mt. Saccarello Italy; adult; thorax muscle
C:Genetics:
A:Genome: mitochondrion
A:Note: ND5
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Query Match 3.7%; Score 7; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 40;

Matches	7;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	20	FIFLFF	26						
Db	157	FIFLFF	163						

RESULT 45

T12154

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Carabus putzeysianus mitochondri

C;Species: mitochondrion Carabus putzeysianus raynaudianus

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Jun-2002

C;Accession: T12154

R;Imura, Y.; Su, Z.H.; Kim, C.G.; Osawa, S.

Elytra 26, 223-248, 1998

A;Title: Reorganization of the Oreocarabus complex (Coleoptera, Carabidae) based on endo

A;Reference number: 217381

A;Accession: T12154

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-355 <IMU>

A;Cross-references: EMBL:AB017448; PIDN:BAA33164.1

A;Experimental source: isolate laghi di Iolalunga Italy; adult; thorax muscle

C;Genetics:

A;Genome: mitochondrion

A;Note: ND5

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match

Best Local Similarity 3.7%; Score 7; DB 2; Length 355;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	20	FIFLFF	26						
Db	157	FIFLFF	163						

Search completed: November 9, 2002, 07:31:26
Job time : 53 secs

THIS PAGE BLANK (USPTO)